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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/998,966

DATE: 01/29/2002
TIME: 15:45:55

Input Set : N:\Crf3\RULE60\09998966.txt
Output Set: N:\CRF3\01292002\I998966.raw

3 <110> APPLICANT: Shimkets, Richard
 4 Fernandes, Elma
 5 Boldog, Ferenc
 7 <120> TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
 9 <130> FILE REFERENCE: 15966-551
 11 <140> CURRENT APPLICATION NUMBER: 09/998,966
 12 <141> CURRENT FILING DATE: 2001-10-31
 14 <150> PRIOR APPLICATION NUMBER: 09/569,269
 15 <151> PRIOR FILING DATE: 2000-05-11
 17 <150> PRIOR APPLICATION NUMBER: 60/134,315
 18 <151> PRIOR FILING DATE: 1999-05-14
 20 <150> PRIOR APPLICATION NUMBER: 60/175,744
 21 <151> PRIOR FILING DATE: 2000-01-12
 23 <150> PRIOR APPLICATION NUMBER: 60/188,274
 24 <151> PRIOR FILING DATE: 2000-03-10
 26 <160> NUMBER OF SEQ ID NOS: 52
 28 <170> SOFTWARE: PatentIn Ver. 2.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 670
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
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 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (130)..(639)
 39 <400> SEQUENCE: 1
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 42 cccgcgcgc gaaggcagag cgcggacgc cgggagcga cgagcgcgcga gcgaaccggg 120
 44 tgccgggtc atg cgc cgc ctg tgg ctg ggc ctg gcc tgg ctg ctg ctg 171
 45 Met Arg Arg Arg Leu Trp Leu Gly Leu Ala Trp Leu Leu Leu
 46 1 5 10
 48 gcg cgg gcg ccg gac gcc gcg gga acc ccg agc gcg tcg cgg gga ccg 219
 49 Ala Arg Ala Pro Asp Ala Ala Gly Thr Pro Ser Ala Ser Arg Gly Pro
 50 15 20 25 30
 52 cgc agc tac ccg cac ctg gag ggc gac gtg cgc tgg cgg cgc ctc ttc 267
 53 Arg Ser Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe
 54 35 40 45
 56 tcc tcc act cac ttc ttc ctg cgc gtg gat ccc ggc ggc cgc gtg cag 315
 57 Ser Ser Thr His Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln
 58 50 55 60
 60 ggc acc cgc tgg cgc cac ggc cag gac agc atc ctg gag atc cgc tct 363
 61 Gly Thr Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser
 62 65 70 75
 64 gta cac gtg ggc gtc gtg gtc atc aaa gca gtg tcc tca ggc ttc tac 411

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65 Val His Val Gly Val Val Val Ile Lys Ala Val Ser Ser Gly Phe Tyr
66 80 85 90
68 gtg gcc atg aac aac cgc cgg ggc cgc ctc tac ggg tcg cga ctc tac acc 459
69 Val Ala Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr
70 95 100 105 110
72 gtg gac tgc agg ttc cgg gag cgc atc gaa gag aac ggc cac aac acc 507
73 Val Asp Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr
74 115 120 125
76 tac gcc tca cag cgc tgg cgc cgc cgc ggc cag ccc atg ttc ctg gcg 555
77 Tyr Ala Ser Gln Arg Trp Arg Arg Arg Gly Gln Pro Met Phe Leu Ala
78 130 135 140
80 ctg gac agg agg ggg ggg ccc cgg cca ggc ggc cgg acg cgg cgg tac 603
81 Leu Asp Arg Arg Gly Gly Pro Arg Pro Gly Gly Arg Thr Arg Arg Tyr
82 145 150 155
84 cac ctg tcc gcc cac ttc ctg ccc gtc ctg gtc tcc tgaggccctg 649
85 His Leu Ser Ala His Phe Leu Pro Val Leu Val Ser
86 160 165 170
88 agaggccggc ggctcccaa g 670
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93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
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101 20 25 30
103 Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe Ser Ser
104 35 40 45
106 Thr His Phe Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln Gly Thr
107 50 55 60
109 Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser Val His
110 65 70 75 80
112 Val Gly Val Val Val Ile Lys Ala Val Ser Ser Gly Phe Tyr Val Ala
113 85 90 95
115 Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr Val Asp
116 100 105 110
118 Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr Tyr Ala
119 115 120 125
121 Ser Gln Arg Trp Arg Arg Arg Gly Gln Pro Met Phe Leu Ala Leu Asp
122 130 135 140
124 Arg Arg Gly Gly Pro Arg Pro Gly Gly Arg Thr Arg Arg Tyr His Leu
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127 Ser Ala His Phe Leu Pro Val Leu Val Ser
128 165 170
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 1680
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens

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136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (177)..(1655)
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145 ggggtgaccc tcggcagatc ttccctgtgg ctttccctgc ccactccagt gacact atg 179
146 Met
147 1
149 cac ccc cac cgt gac ccg aga ggc ctc tgg ctc ctg ctg ccg tcc ttg 227
150 His Pro His Arg Asp Pro Arg Gly Leu Trp Leu Leu Leu Pro Ser Leu
151 5 10 15
153 tcc ctg ctg ctt ttt gag gtg gcc aga gct ggc cga gcc gtg gtt agc 275
154 Ser Leu Leu Leu Phe Glu Val Ala Arg Ala Gly Arg Ala Val Val Ser
155 20 25 30
157 tgt cct gcc gcc tgc ttg tgc gcc agc aac atc ctc agc tgc tcc aag 323
158 Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser Lys
159 35 40 45
161 cag cag ctg ccc aat gtg ccc cat tcc ttg ccc agt tac aca gca cta 371
162 Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala Leu
163 50 55 60 65
165 ctg gac ctc agt cac aac aac ctg agc cgc ctg cgg gcc gag tgg acc 419
166 Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp Thr
167 70 75 80
169 ccc acg cgc ctg acc caa ctg cac tcc ctg ctg agc cac aac cac 467
170 Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn His
171 85 90 95
173 ctg aac ttc atc tcc tct gag gcc ttt tcc ccg gta ccc aac ctg cgc 515
174 Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu Arg
175 100 105 110
177 tac ctg gac ctc tcc tcc aac cag ctg cgt aca ctg gat gag ttc ctg 563
178 Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe Leu
179 115 120 125
181 ttc agt gac ctg caa gta ctg gag gtg ctg ctg ctc tac aat aac cac 611
182 Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Leu Tyr Asn Asn His
183 130 135 140 145
185 atc atg gcg gtg gac cgg tgc gcc ttc gat gac atg gcc cag ctg cag 659
186 Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu Gln
187 150 155 160
189 aaa ctc tac ttg agc cag aac cag atc tct cgc ttc cct ctg gaa ctg 707
190 Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu Leu
191 165 170 175
193 gtc aag gaa gga gcc aag cta ccc aaa cta acg ctc ctg gat ctc tct 755
194 Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu Ser
195 180 185 190
197 tct aac aag ctg aag aac ttg cca ttg cct gac ctg cag aag ctg ccc 803
198 Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu Pro
199 195 200 205
201 gcc tgg atc aag aat ggg ctg tac cta cat aac aac ccc ctg aac tgc 851

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202	Ala	Trp	Ile	Lys	Asn	Gly	Leu	Tyr	Leu	His	Asn	Asn	Pro	Leu	Asn	Cys	
203	210				215				220							225	
205	gac	tgt	gag	ctc	tac	cag	ctg	ttt	tca	cac	tgg	cag	tat	cgg	cag	ctg	899
206	Asp	Cys	Glu	Leu	Tyr	Gln	Leu	Phe	Ser	His	Trp	Gln	Tyr	Arg	Gln	Leu	
207								230			235					240	
209	agc	tcc	gtg	atg	gac	ttt	caa	gag	gat	ctg	tac	tgc	atg	aac	tcc	aag	947
210	Ser	Ser	Val	Met	Asp	Phe	Gln	Glu	Asp	Leu	Tyr	Cys	Met	Asn	Ser	Lys	
211								245			250					255	
213	aag	ctg	cac	aat	gtc	tcc	aac	ctg	agt	ttc	ctc	aac	tgt	ggc	gag	tac	995
214	Lys	Leu	His	Asn	Val	Phe	Asn	Leu	Ser	Phe	Leu	Asn	Cys	Gly	Glu	Tyr	
215								260			265					270	
217	aag	gag	cgt	gcc	tgg	gag	gcc	cac	ctg	ggt	gac	acc	ttg	atc	atc	aag	1043
218	Lys	Glu	Arg	Ala	Trp	Glu	Ala	His	Leu	Gly	Asp	Thr	Leu	Ile	Ile	Lys	
219								275			280					285	
221	tgt	gac	acc	aag	cag	caa	ggg	atg	acc	aag	gtg	tgg	gtg	aca	cca	agt	1091
222	Cys	Asp	Thr	Lys	Gln	Gln	Gly	Met	Thr	Lys	Val	Trp	Val	Thr	Pro	Ser	
223								290			295					300	305
225	aat	gaa	cgg	gtg	cta	gat	gag	gtg	acc	aat	ggc	aca	gtg	agt	gtg	tct	1139
226	Asn	Glu	Arg	Val	Leu	Asp	Glu	Val	Thr	Asn	Gly	Thr	Val	Ser	Val	Ser	
227								310			315					320	
229	aag	gat	ggc	agt	ctt	ctt	ttc	cag	cag	gtg	cag	gtc	gag	gac	ggt	ggt	1187
230	Lys	Asp	Gly	Ser	Leu	Leu	Phe	Gln	Gln	Val	Gln	Val	Glu	Asp	Gly	Gly	
231								325			330					335	
233	gtg	tat	acc	tgc	tat	gcc	atg	gga	gag	act	ttc	aat	gag	aca	ctg	tct	1235
234	Val	Tyr	Thr	Cys	Tyr	Ala	Met	Gly	Glu	Thr	Phe	Asn	Glu	Thr	Leu	Ser	
235								340			345					350	
237	gtg	gaa	ttg	aaa	gtg	cac	aat	ttc	acc	ttg	cac	gga	cac	cat	gac	acc	1283
238	Val	Glu	Leu	Lys	Val	His	Asn	Phe	Thr	Leu	His	Gly	His	His	Asp	Thr	
239								355			360					365	
241	ctc	aac	aca	gcc	tat	acc	acc	cta	gtg	ggc	tgt	atc	ctt	agt	gtg	gtc	1331
242	Leu	Asn	Thr	Ala	Tyr	Thr	Thr	Leu	Val	Gly	Cys	Ile	Leu	Ser	Val	Val	
243								370			375					380	385
245	ctg	gtc	ctc	ata	tac	tac	ctc	acc	cct	tgc	cgc	tgc	tgg	tgc	cg	1379	
246	Leu	Val	Leu	Ile	Tyr	Leu	Tyr	Leu	Thr	Pro	Cys	Arg	Cys	Trp	Cys	Arg	
247								390			395					400	
249	ggt	gta	gag	aag	cct	tcc	agc	cat	caa	gga	gac	agc	ctc	agc	tct	tcc	1427
250	Gly	Val	Glu	Lys	Pro	Ser	Ser	His	Gln	Gly	Asp	Ser	Leu	Ser	Ser	Ser	
251								405			410					415	
253	atg	ctt	agt	acc	aca	ccc	aac	cat	gat	cct	atg	gct	ggt	ggg	gac	aaa	1475
254	Met	Leu	Ser	Thr	Thr	Pro	Asn	His	Asp	Pro	Met	Ala	Gly	Gly	Asp	Lys	
255								420			425					430	
257	gat	gat	ggt	ttt	gac	cg	cg	gt	gct	ttc	ctg	gaa	cct	gct	gga	cct	1523
258	Asp	Asp	Gly	Phe	Asp	Arg	Arg	Val	Ala	Phe	Leu	Glu	Pro	Ala	Gly	Pro	
259								435			440					445	
261	ggg	cag	ggt	caa	aac	gg	aag	ctc	aag	cca	gg	aac	acc	ctg	cca	gt	1571
262	Gly	Gln	Gly	Gln	Asn	Gly	Lys	Leu	Lys	Pro	Gly	Asn	Thr	Leu	Pro	Val	
263								450			455					460	465
265	cct	gag	gcc	aca	ggc	aag	ggc	caa	cg	agg	atg	tgc	gat	cca	gaa	tca	1619
266	Pro	Glu	Ala	Thr	Gly	Lys	Gln	Arg	Arg	Met	Ser	Asp	Pro	Glu	Ser		

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267 470 475 480
269 gtc agc tcg gtc ttc tct gat acg ccc att gtg gtg tgagcaggat 1665
270 Val Ser Ser Val Phe Ser Asp Thr Pro Ile Val Val
271 485 490
273 ggggtggtgg ggaga 1680
276 <210> SEQ ID NO: 4
277 <211> LENGTH: 493
278 <212> TYPE: PRT
279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 4
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285 Leu Ser Leu Leu Leu Phe Glu Val Ala Arg Ala Gly Arg Ala Val Val
286 20 25 30
288 Ser Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser
289 35 40 45
291 Lys Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala
292 50 55 60
294 Leu Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp
295 65 70 75 80
297 Thr Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn
298 85 90 95
300 His Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu
301 100 105 110
303 Arg Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe
304 115 120 125
306 Leu Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Leu Tyr Asn Asn
307 130 135 140
309 His Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu
310 145 150 155 160
312 Gln Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu
313 165 170 175
315 Leu Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu
316 180 185 190
318 Ser Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu
319 195 200 205
321 Pro Ala Trp Ile Lys Asn Gly Leu Tyr Leu His Asn Asn Pro Leu Asn
322 210 215 220
324 Cys Asp Cys Glu Leu Tyr Gln Leu Phe Ser His Trp Gln Tyr Arg Gln
325 225 230 235 240
327 Leu Ser Ser Val Met Asp Phe Gln Glu Asp Leu Tyr Cys Met Asn Ser
328 245 250 255
330 Lys Lys Leu His Asn Val Phe Asn Leu Ser Phe Leu Asn Cys Gly Glu
331 260 265 270
333 Tyr Lys Glu Arg Ala Trp Glu Ala His Leu Gly Asp Thr Leu Ile Ile
334 275 280 285
336 Lys Cys Asp Thr Lys Gln Gln Gly Met Thr Lys Val Trp Val Thr Pro
337 290 295 300
339 Ser Asn Glu Arg Val Leu Asp Glu Val Thr Asn Gly Thr Val Ser Val

VERIFICATION SUMMARY
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L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1996 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE: